



## SEQUENCE LISTING

<110> Yeatman, Timothy J.  
Irby, Rosalyn B.

<120> Mutated SRC Oncogene Composition and Methods

<130> USF-T136

<140> US 09/444,711

<141> 1999-11-24

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 1611

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)..(1611)

<223> nucleotide sequence of normal c-Src oncogene coding region

<220>

<221> CDS

<222> (1)..(1611)

<223>

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agc ctg gag ccc gcc gag aac gtg cac ggc gct ggc ggg ggc gct ttc 96  
Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
20 25 30

ccc gcc tcg cag acc ccc agc aag cca gcc tcg gcc gac ggc cac cgc 144  
Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
35 40 45

ggc ccc agc gcg gcc ttc gcc ccc gcg gcc gcc gag ccc aag ctg ttc 192  
Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
50 55 60

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gga ggc ttc aac tcc tcg gac acc gtc acc tcc ccg cag agg gcg ggc 240  
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 65 70 75 80

ccg ctg gcc ggt gga gtg acc acc ttt gtg gcc ctc tat gac tat gag 288  
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
 85 90 95

tct agg acg gag aca gac ctg tcc ttc aag aaa ggc gag cgg ctc cag 336  
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
 100 105 110

att gtc aac aac acg gag gga gac tgg tgg ctg gcc cac tcg ctc agc 384  
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
 115 120 125

aca gga cag aca ggc tac atc ccc agc aac tac gtg gcg ccc tcc gac 432  
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
 130 135 140

tcc atc cag gct gag gag tgg tat ttt ggc aag atc acc aga cgg gag 480  
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
 145 150 155 160

tca gag cgg tta ctg ctc aat gca gag aac ccg aga ggg acc ttc ctc 528  
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
 165 170 175

gtg cga gaa agt gag acc acg aaa ggt gcc tac tgc ctc tca gtg tct 576  
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
 180 185 190

gag ttc gac aac gcc aag ggc ctc aac gtg aag cac tac aag atc cgc 624  
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
 195 200 205

aag ctg gac agc ggc ggc ttc tac atc acc tcc cgc acc cag ttc aac 672  
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
 210 215 220

agc ctg cag cag ctg gtg gcc tac tac tcc aaa cac gcc gat ggc ctg 720  
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
 225 230 235 240

tgc cac cgc ctc acc acc gtg tgc ccc acg tcc aag ccg cag act cag 768  
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
 245 250 255

ggc ctg gcc aag gat gcc tgg gag atc cct cgg gag tcg ctg cgg ctg 816  
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
 260 265 270

gag gtc aag ctg ggc cag ggc tgc ttt ggc gag gtg tgg atg ggg acc	864
Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr	
275 280 285	
tgg aac ggt acc acc agg gtg gcc atc aaa acc ctg aag cct ggc acg	912
Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr	
290 295 300	
atg tct cca gag gcc ttc ctg cag gag gcc cag gtc atg aag aag ctg	960
Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu	
305 310 315 320	
agg cat gag aag ctg gtg cag ttg tat gct gtg gtt tca gag gag ccc	1008
Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro	
325 330 335	
att tac atc gtc acg gag tac atg agc aag ggg agt ttg ctg gac ttt	1056
Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe	
340 345 350	
ctc aag ggg gag aca ggc aag tac ctg cgg ctg cct cag ctg gtg gac	1104
Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp	
355 360 365	
atg gct gct cag atc gcc tca ggc atg gcg tac gtg gag cgg atg aac	1152
Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn	
370 375 380	
tac gtc cac cgg gac ctt cgt gca gcc aac atc ctg gtg gga gag aac	1200
Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn	
385 390 395 400	
ctg gtg tgc aaa gtg gcc gac ttt ggg ctg gct cgg ctc att gaa gac	1248
Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp	
405 410 415	
aat gag tac acg gcg cgg caa ggt gcc aaa ttc ccc atc aag tgg acg	1296
Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr	
420 425 430	
gct cca gaa gct gcc ctc tat ggc cgc ttc acc atc aag tcg gac gtg	1344
Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val	
435 440 445	
tgg tcc ttc ggg atc ctg ctg act gag ctc acc aca aag gga cgg gtg	1392
Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val	
450 455 460	
ccc tac cct ggg atg gtg aac cgc gag gtg ctg gac cag gtg gag cgg	1440
Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg	
465 470 475 480	
ggc tac cgg atg ccc tgc ccg ccg gag tgt ccc gag tcc ctg cac gac	1488
Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp	
485 490 495	

ctc atg tgc cag tgc tgg cgg aag gag cct gag gag cgg ccc acc ttc 1536  
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe  
                   500                                  505                                  510

gag tac ctg cag gcc ttc ctg gag gac tac ttc acg tcc acc gag ccc 1584  
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
                   515                                  520                                  525

cag tac cag ccc ggg gag aac ctc tag 1611  
 Gln Tyr Gln Pro Gly Glu Asn Leu  
                   530                                  535

<210> 2  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(536)  
 <223> amino acid sequence of non-receptor tyrosine kinase encoded  
           by the normal c-Src coding region

<400> 2  
 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
 1                                  5                                  10                                  15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
                   20                                  25                                  30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
                   35                                  40                                  45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
                   50                                  55                                  60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 65                                  70                                  75                                  80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
                   85                                  90                                  95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
                   100                                  105                                  110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
                   115                                  120                                  125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
                   130                                  135                                  140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
 145                                  150                                  155                                  160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
 165 170 175  
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
 180 185 190  
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
 195 200 205  
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
 210 215 220  
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
 225 230 235 240  
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
 245 250 255  
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
 260 265 270  
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
 275 280 285  
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr  
 290 295 300  
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu  
 305 310 315 320  
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
 325 330 335  
 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe  
 340 345 350  
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp  
 355 360 365  
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  
 370 375 380  
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn  
 385 390 395 400  
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
 405 410 415  
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
 420 425 430  
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val  
 435 440 445  
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val  
 450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg  
465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp  
485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe  
500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535

<210> 3  
<211> 1611  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(1593)  
<223> nucleotide sequence of mutant c-Src oncogene coding region

<220>  
<221> CDS  
<222> (1)..(1593)  
<223>

<220>  
<221> misc\_feature  
<222> (1591)..(1591)  
<223> Point mutation in normal c-Src causes transition from c-->t and the formation of a stop codon.

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Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
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agc ctg gag ccc gcc gag aac gtg cac ggc gct ggc ggg ggc gct ttc 96  
Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
20 25 30  
  
ccc gcc tcg cag acc ccc agc aag cca gcc tcg gcc gac ggc cac cgc 144  
Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
35 40 45  
  
ggc ccc agc gcg gcc ttc gcc ccc gcg gcc gcc gag ccc aag ctg ttc 192  
Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
50 55 60

gga ggc ttc aac tcc tcg gac acc gtc acc tcc ccg cag agg gcg ggc 240  
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 65 70 75 80

ccg ctg gcc ggt gga gtg acc acc ttt gtg gcc ctc tat gac tat gag 288  
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
 85 90 95

tct agg acg gag aca gac ctg tcc ttc aag aaa ggc gag cgg ctc cag 336  
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
 100 105 110

att gtc aac aac acg gag gga gac tgg tgg ctg gcc cac tcg ctc agc 384  
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
 115 120 125

aca gga cag aca ggc tac atc ccc agc aac tac gtg gcg ccc tcc gac 432  
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
 130 135 140

tcc atc cag gct gag gag tgg tat ttt ggc aag atc acc aga cgg gag 480  
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
 145 150 155 160

tca gag cgg tta ctg ctc aat gca gag aac ccg aga ggg acc ttc ctc 528  
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
 165 170 175

gtg cga gaa agt gag acc acg aaa ggt gcc tac tgc ctc tca gtg tct 576  
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
 180 185 190

gag ttc gac aac gcc aag ggc ctc aac gtg aag cac tac aag atc cgc 624  
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
 195 200 205

aag ctg gac agc ggc ggc ttc tac atc acc tcc cgc acc cag ttc aac 672  
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
 210 215 220

agc ctg cag cag ctg gtg gcc tac tac tcc aaa cac gcc gat ggc ctg 720  
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
 225 230 235 240

tgc cac cgc ctc acc acc gtg tgc ccc acg tcc aag ccg cag act cag 768  
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
 245 250 255

ggc ctg gcc aag gat gcc tgg gag atc cct cgg gag tcg ctg cgg ctg 816  
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
 260 265 270

gag gtc aag ctg ggc cag ggc tgc ttt ggc gag gtg tgg atg ggg acc 864  
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
 275 280 285

tgg aac ggt acc acc agg gtg gcc atc aaa acc ctg aag cct ggc acg	912
Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr	
290 295 300	
atg tct cca gag gcc ttc ctg cag gag gcc cag gtc atg aag aag ctg	960
Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu	
305 310 315 320	
agg cat gag aag ctg gtg cag ttg tat gct gtg gtt tca gag gag ccc	1008
Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro	
325 330 335	
att tac atc gtc acg gag tac atg agc aag ggg agt ttg ctg gac ttt	1056
Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe	
340 345 350	
ctc aag ggg gag aca ggc aag tac ctg cgg ctg cct cag ctg gtg gac	1104
Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp	
355 360 365	
atg gct gct cag atc gcc tca ggc atg gcg tac gtg gag cgg atg aac	1152
Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn	
370 375 380	
tac gtc cac cgg gac ctt cgt gca gcc aac atc ctg gtg gga gag aac	1200
Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn	
385 390 395 400	
ctg gtg tgc aaa gtg gcc gac ttt ggg ctg gct cgg ctc att gaa gac	1248
Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp	
405 410 415	
aat gag tac acg gcg cgg caa ggt gcc aaa ttc ccc atc aag tgg acg	1296
Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr	
420 425 430	
gct cca gaa gct gcc ctc tat ggc cgc ttc acc atc aag tcg gac gtg	1344
Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val	
435 440 445	
tgg tcc ttc ggg atc ctg ctg act gag ctc acc aca aag gga cgg gtg	1392
Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val	
450 455 460	
ccc tac cct ggg atg gtg aac cgc gag gtg ctg gac cag gtg gag cgg	1440
Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg	
465 470 475 480	
ggc tac cgg atg ccc tgc ccg ccg gag tgt ccc gag tcc ctg cac gac	1488
Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp	
485 490 495	
ctc atg tgc cag tgc tgg cgg aag gag cct gag gag cgg ccc acc ttc	1536
Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe	
500 505 510	



gag tac ctg cag gcc ttc ctg gag gac tac ttc acg tcc acc gag ccc 1584  
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
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cag tac tag cccggggaga acctctag 1611  
 Gln Tyr  
       530

<210> 4  
 <211> 530  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> (1)..(530)  
 <223> amino acid sequence of the mutant c-Src polypeptide encoded  
       by the mutant c-Src coding region

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           20                          25                          30  
 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
           35                          40                          45  
 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
           50                          55                          60  
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
           65                          70                          75                          80  
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
                   85                          90                          95  
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
           100                          105                          110  
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
           115                          120                          125  
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
           130                          135                          140  
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
           145                          150                          155                          160  
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
                   165                          170                          175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
 180 185 190  
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
 195 200 205  
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
 210 215 220  
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
 225 230 235 240  
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
 245 250 255  
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
 260 265 270  
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
 275 280 285  
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr  
 290 295 300  
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu  
 305 310 315 320  
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
 325 330 335  
 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe  
 340 345 350  
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp  
 355 360 365  
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  
 370 375 380  
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn  
 385 390 395 400  
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
 405 410 415  
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
 420 425 430  
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val  
 435 440 445  
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val  
 450 455 460  
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg  
 465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp  
                                     485                                    490                                    495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe  
                                     500                                    505                                    510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
                                     515                                    520                                    525

Gln Tyr  
           530

<210> 5  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 3' mutant allele specific primer  
 <220>  
 <221> misc\_feature

<222> (15)..(15)  
 <223> n is defined as a 3-nitropyrrole residue

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 tagaggttct ccccnnggcta

20

<210> 6  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 3' wild-type allele specific primer

<400> 6  
 tagaggttct ccccgggctg

20

<210> 7  
 <211> 164  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Antisense sequence complementary to 5' region of c-Src gene

&lt;400&gt; 7

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tgaagcacta caagatccgc aagctggaca gcggcggctt ctacatcacc tcccgcaccc 120

agttcaacag cctgcagcag ctggtggcct actactccag tgag 164